In the Claims

Claim 1 is cancelled and the following new claims are added to read as follows:

2. (New) A method for assessing toxicity and toxicology of a compound, comprising:

a) exposing a set of genes to a compound;

b) monitoring the response of each gene in the set of genes to the compound;

c) creating gene expression profiles using two or more variables;

d) creating composite variables from the gene expression profiles of (c);

e) creating one composite from the composite variables of (d); and

f) comparing the results of (e) to a profile of a known compound.

3. (New) The method of Claim 2, wherein the set of genes comprises 10-100,000 genes.

4. (New) The method of Claim 2, wherein the variables are time, treatment or dose.

5. (New) The method of Claim 4, wherein the variables of (c) are dose and time.

6. (New) The method of Claim 2, wherein the response of the genes is averaged.

7. (New) The method of Claim 2, wherein the gene expression profiles are created using contrast analysis.

8. (New) The method of Claim 2, wherein the gene expression profiles are created using cluster analysis.

9. (New) The method of Claim 2, wherein the gene expression profiles of (d) are created using principal component analysis, partial least squares, or factor analysis.

10. (New) The method of Claim 2, wherein the composite variables of (e) are created using logistic regression, or discriminant analysis.

11. (New) A method for screening a compound for a toxicological effect, comprising

(a) selecting a plurality of polynucleotide targets wherein the polynucleotide targets have a first gene expression levels altered in tissues treated with known toxicological agents;

(b) treating a second tissue sample with a compound to be tested to induce second gene expression levels of a plurality of polynucleotide;

(c) comparing the first expression level of (a) with the second expression level of (b).

12. (New) The method of Claim 11, wherein the similarity of the first expression level to the second expression level correlates with a toxicological effect.

13. (New) The method of Claim 11, wherein the tissue samples are liver, kidney, brain, spleen, pancreas and lung.

14. (New) The method of Claim 11, wherein the known toxicological agent is acetaminophen.

15. (New) The method of Claim 11, wherein the known toxicological agent is CCl_4.

16. (New) A method for monitoring the expression of a multiplicity of genes comprising

(a) providing a pool of target nucleic acids comprising mRNA transcripts of one or more genes;

(b) hybridizing the pool of nucleic acids to an array of oligonucleotide probes fixed to a surface;

(c) quantifying the hybridized nucleic acids in the array.

17. (New) The array of Claim 16, wherein the array comprises 400,000 different oligonucleotide probes per cm^2.

18. (New) The method of Claim 16, wherein the oligonucleotide arrays are synthesized by very large scale immobilized polymer synthesis.

19. (New) The method of Claim 16, wherein the target nucleic acids are labeled.

20. (New) The method of Claim 19, wherein the target nucleic acids are labeled prior to hybridization.

21. (New) The method of Claim 16, wherein the oligonucleotides in the array are paired target specific oligonucleotides.

22. (New) A method for monitoring message levels of a multiplicity of pre-selected genes in the presence of a large abundance of non-target nucleic acids comprising the use of high density oligonucleotide arrays.